

## SEQUENCE LISTING

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&lt;160&gt; 48

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&lt;210&gt; 1

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 1

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&lt;213&gt; Artificial sequence

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&lt;220&gt;

&lt;223&gt; Primer

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&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 5

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&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 6

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&lt;210&gt; 7

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&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

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<400> 9  
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ctcctttaa ctacttaatt acattcattt aaaaagaaaa cctattcact gcctgtcctg 1500  
tggacagaca gatatgca 1518

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<220>  
<223> Estrogen Receptor Target Recognition Sequence

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<210> 15  
<211> 828  
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<220>  
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<220>  
<221> CDS

&lt;222&gt; (1)..(828)

&lt;223&gt;

&lt;400&gt; 15

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| atg gta aag aac ccg aat ccg gtg ttc act ccc cgt gaa ggt gcc gga | 48 |
| Met Val Lys Asn Pro Asn Pro Val Phe Thr Pro Arg Glu Gly Ala Gly |    |
| 1 5 10 15   |    |

|   |    |
|---|----|
| acg ccg aag ttc cgc gaa aaa ccg atg gaa aag gcg gtg ggc ctc acc | 96 |
| Thr Pro Lys Phe Arg Glu Lys Pro Met Glu Lys Ala Val Gly Leu Thr |    |
| 20 25 30  |    |

|   |     |
|---|-----|
| tcc cgt ttt gat ttc gcc att cat gtg gcg cat gcc cgt tcc cgt ggt | 144 |
| Ser Arg Phe Asp Phe Ala Ile His Val Ala His Ala Arg Ser Arg Gly |     |
| 35 40 45  |     |

|   |     |
|---|-----|
| ctg cgt cgg cgc atg cca ccg gtg ctg cgt cga cgg gct att gat gcg | 192 |
| Leu Arg Arg Arg Met Pro Pro Val Leu Arg Arg Arg Ala Ile Asp Ala |     |
| 50 55 60  |     |

|   |     |
|---|-----|
| ctg ctg cag ggg ctg tgt ttc cac tat gac ccg ctg gcc aac cgc gtc | 240 |
| Leu Leu Gln Gly Leu Cys Phe His Tyr Asp Pro Leu Ala Asn Arg Val |     |
| 65 70 75 80   |     |

|   |     |
|---|-----|
| cag tgt tcc atc acc aca ctg gcc att gag tgc gga ctg gcg aca gag | 288 |
| Gln Cys Ser Ile Thr Thr Leu Ala Ile Glu Cys Gly Leu Ala Thr Glu |     |
| 85 90 95  |     |

|   |     |
|---|-----|
| tcc ggt gca gga aaa ctc tcc atc acc cgt gcc acc cgg gcc ctg acg | 336 |
| Ser Gly Ala Gly Lys Leu Ser Ile Thr Arg Ala Thr Arg Ala Leu Thr |     |
| 100 105 110   |     |

|   |     |
|---|-----|
| ttc ctg tca gag ctg gga ctg att acc tac cag acg gaa tat gac ccg | 384 |
| Phe Leu Ser Glu Leu Gly Leu Ile Thr Tyr Gln Thr Glu Tyr Asp Pro |     |
| 115 120 125   |     |

|   |     |
|---|-----|
| ctt atc ggg tgc tac att ccg acc gac atc acg ttc aca ctg gct ctg | 432 |
| Leu Ile Gly Cys Tyr Ile Pro Thr Asp Ile Thr Phe Thr Leu Ala Leu |     |
| 130 135 140   |     |

|   |     |
|---|-----|
| ttt gct gcc ctt gat gtg tct gag gat gca gtg gca gct gcg cgc cgc | 480 |
| Phe Ala Ala Leu Asp Val Ser Glu Asp Ala Val Ala Ala Arg Arg     |     |
| 145 150 155 160   |     |

|   |     |
|---|-----|
| agt cgt gtt gaa tgg gaa aac aaa cag cgc aaa aag cag ggg ctg gat | 528 |
| Ser Arg Val Glu Trp Glu Asn Lys Gln Arg Lys Lys Gln Gly Leu Asp |     |
| 165 170 175   |     |

|   |     |
|---|-----|
| acc ctg ggt atg gat gag ctg ata gcg aaa gcc tgg cgt ttt gtg cgt | 576 |
| Thr Leu Gly Met Asp Glu Leu Ile Ala Lys Ala Trp Arg Phe Val Arg |     |
| 180 185 190   |     |

gag cgt ttc cgc agt tac cag aca gag ctt cag tcc cgt gga ata aaa 624  
 Glu Arg Phe Arg Ser Tyr Gln Thr Glu Leu Gln Ser Arg Gly Ile Lys  
 195 200 205

cgt gcc cgt gcg cgt cgt gat gcg aac aga gaa cgt cag gat atc gtc 672  
 Arg Ala Arg Ala Arg Arg Asp Ala Asn Arg Glu Arg Gln Asp Ile Val  
 210 215 220

acc cta gtg aaa cgg cag ctg acg cgt gaa atc tcg gaa gga cgc ttc 720  
 Thr Leu Val Lys Arg Gln Leu Thr Arg Glu Ile Ser Glu Gly Arg Phe  
 225 230 235 240

act gct aat ggt gag gcg gta aaa cgc gaa gtg gag cgt cgt gtg aag 768  
 Thr Ala Asn Gly Glu Ala Val Lys Arg Glu Val Glu Arg Arg Val Lys  
 245 250 255

gag cgc atg att ctg tca cgt aac cgc aat tac agc cgg ctg gcc aca 816  
 Glu Arg Met Ile Leu Ser Arg Asn Arg Asn Tyr Ser Arg Leu Ala Thr  
 260 265 270

gct tct ccc tga 828  
 Ala Ser Pro.  
 275

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 <212> PRT  
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 <223> repA sequence

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Thr Pro Lys Phe Arg Glu Lys Pro Met Glu Lys Ala Val Gly Leu Thr  
 20 25 30

Ser Arg Phe Asp Phe Ala Ile His Val Ala His Ala Arg Ser Arg Gly  
 35 40 45

Leu Arg Arg Arg Met Pro Pro Val Leu Arg Arg Arg Ala Ile Asp Ala  
 50 55 60

Leu Leu Gln Gly Leu Cys Phe His Tyr Asp Pro Leu Ala Asn Arg Val  
 65 70 75 80

8

Gln Cys Ser Ile Thr Thr Leu Ala Ile Glu Cys Gly Leu Ala Thr Glu  
                             85                            90                            95  
 Ser Gly Ala Gly Lys Leu Ser Ile Thr Arg Ala Thr Arg Ala Leu Thr  
                             100                            105                            110  
 Phe Leu Ser Glu Leu Gly Leu Ile Thr Tyr Gln Thr Glu Tyr Asp Pro  
                             115                            120                            125  
 Leu Ile Gly Cys Tyr Ile Pro Thr Asp Ile Thr Phe Thr Leu Ala Leu  
                             130                            135                            140  
 Phe Ala Ala Leu Asp Val Ser Glu Asp Ala Val Ala Ala Ala Arg Arg  
                             145                            150                            155                            160  
 Ser Arg Val Glu Trp Glu Asn Lys Gln Arg Lys Lys Gln Gly Leu Asp  
                             165                            170                            175  
 Thr Leu Gly Met Asp Glu Leu Ile Ala Lys Ala Trp Arg Phe Val Arg  
                             180                            185                            190  
 Glu Arg Phe Arg Ser Tyr Gln Thr Glu Leu Gln Ser Arg Gly Ile Lys  
                             195                            200                            205  
 Arg Ala Arg Ala Arg Arg Asp Ala Asn Arg Glu Arg Gln Asp Ile Val  
                             210                            215                            220  
 Thr Leu Val Lys Arg Gln Leu Thr Arg Glu Ile Ser Glu Gly Arg Phe  
                             225                            230                            235                            240  
 Thr Ala Asn Gly Glu Ala Val Lys Arg Glu Val Glu Arg Arg Val Lys  
                             245                            250                            255  
 Glu Arg Met Ile Leu Ser Arg Asn Arg Asn Tyr Ser Arg Leu Ala Thr  
                             260                            265                            270  
 Ala Ser Pro  
                             275

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 cgggtgcacaa aaaaacagcg tcgcatgcaa aaaacaatct catcatccac ctctggagc 120



atccgattcc ccctgttttt aatacaaaat acgcctcagc gacggggaat tt 172

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<211> 195

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<400> 18

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aagcgccagc cgccagtctt acagggtgca atgtatcttt taaacacctg tttatatctc 120

ctttaaacta ctttaattaca ttcatttaaa aagaaaacct attcactgcc tgtcctgtgg 180

acagacagat atgca 195

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<212> DNA

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<220>

<223> Primer

<400> 19

aattccccgt cgctgaggcg 20

<210> 20

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 20

cgtaagccgg tactgattga 20

<210> 21

<211> 110

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<220>

<223> Primer

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<223> n = a, g, c or t

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<222> (56)..(57)

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<222> (59)..(60)

<223> n = a, g, c or t

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<222> (62)..(63)

<223> n = a, g, c or t

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<223> Primer

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<210> 24

<211> 2390

<212> DNA

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<223> TAC-V5-REPA-CIS-ORI-408 construct

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gttggaatg taattcagct ccgccatcgc cgcttccact ttttccgcg ttttcgcaga 180

|             |            |             |             |             |             |      |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| aacgtggctg  | gcctggttca | ccacgcggga  | aacggctctga | taagagacac  | cggcatactc  | 240  |
| tgcgacatcg  | tataacgtta | ctggtttcac  | attcaccacc  | ctgaattgac  | tctcttcgg   | 300  |
| gcgctatcat  | gccataccgc | gaaaggtttt  | gcaccattcg  | gctagcgatg  | accctgctga  | 360  |
| ttggttcgct  | gaccatttcc | ggggtgcgga  | acggcggttac | cagaaactca  | gaagggttcgt | 420  |
| ccaaccaaac  | cgactctgac | ggcagtttac  | gagagagatg  | atagggtctg  | cttcagtaag  | 480  |
| ccagatgcta  | cacaattagg | cttgatcata  | ttgtcgttag  | aacgcggcta  | caattaatac  | 540  |
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| cattcatgtg  | gcgcatgccc | gttcgcgtgg  | tctgcgtcga  | cgcatgccac  | cagtgcgtgc  | 960  |
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| ccgctccag   | tgctccatca | ccacgctggc  | cattgagtcg  | ggactggcga  | cggagtcctgc | 1080 |
| tgccggaâaa  | ctctccatca | cccgtgccac  | ccgggccctg  | acgttcctgt  | cagagctggg  | 1140 |
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| tcagacagag  | cttaagtccc | ggggaataaa  | gcgtgccctg  | gcgcgtcgtg  | atgcggacag  | 1440 |
| ggaacgtcag  | gatattgtca | ccctggtgaa  | acggcagctg  | acgcgcgaaa  | tcgcggaagg  | 1500 |
| gcgcttcaact | gccaatcgtg | aggcggtaaa  | acgcgaagtt  | gagcgtcgtg  | tgaaggagcg  | 1560 |
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| acctcctctg  | aataatccgg | cctgcgccgg  | aggcttccgc  | acgtctgaag  | cccgcagcgc  | 1680 |
| cacaaaaaat  | cagcaccaca | tacaaaaaac  | aacctcatca  | tccagcttct  | ggtgcatccg  | 1740 |
| gccccccctg  | ttttcgatac | aaaacacgcc  | tcacagacgg  | ggaattttgc  | ttatccacat  | 1800 |
| taaactgcaa  | gggacttccc | cataagggtta | caaccgttca  | tgtcataaag  | cgccatccgc  | 1860 |
| cagcgttaca  | gggtgcaatg | tatcttttaa  | acacctgttt  | atatctcctt  | taaactactt  | 1920 |
| aattacattc  | atttaaaaag | aaaacctatt  | cactgcctgt  | cctgtggaca  | gacagatatg  | 1980 |
| cacctccac   | cgcaagcggc | gggcccctac  | cggagccgct  | ttagttacaa  | cactcagaca  | 2040 |
| caaccaccag  | aaaaaccccg | gtccagcgca  | gaactgaaac  | cacaaagccc  | ctccctcata  | 2100 |
| actgaaaagc  | ggccccgccc | cggcccgaag  | ggccggaaca  | gagtcgcttt  | taattatgaa  | 2160 |
| tggtgtaact  | acttcatcat | cgctgtcagt  | cttctcgtcg  | gaagttctca  | gtacacgctc  | 2220 |
| gtaagcggcc  | ctgacggccc | gctaacgcgg  | agatacggcc  | cgacttcggg  | taaaccctcg  | 2280 |
| tcgggaccac  | tccgaccgcg | cacagaagct  | ctctcatggc  | tgaaagcggg  | tatggtctgg  | 2340 |
| cagggctggg  | gatgggtaag | gtgaaatcta  | tcaatcagta  | ccggcttacg  |             | 2390 |

&lt;210&gt; 25

&lt;211&gt; 2384

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; TAC-NNB-REPA-CIS-ORI-408 construct

&lt;220&gt;

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&lt;222&gt; (695)..(696)

&lt;223&gt; n = a, g, c or t

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 gttgggaatg taattcagct ccgccatcgc cgcttccact ttttcccgcg ttttcgcaga 180  
 aacgtggctg gcctggttca ccacgcggga aacggtctga taagagacac cggcatactc 240  
 tgcgacatcg tataacgtta ctggtttcac attcaccacc ctgaattgac tctcttccg 300  
 gcgctatcat gccataccgc gaaagggttt gcaccattcg gctagcgatg accctgctga 360  
 ttggttcgct gaccatttcc ggggtgcgga acggcggttac cagaaactca gaagggttcgt 420  
 ccaaccaaac cgactctgac ggcagtttac gagagagatg atagggtctg cttcagtaag 480  
 ccagatgcta cacaattagg cttgtacata ttgtcgtag aacgcggcta caattaatac 540  
 ataaccttat gtatcataca catacgattt aggtgacact atagaataca agcttactcc 600  
 ccatccccct gttgacaatt aatcatggct cgtataatgt gtggaattgt gagcggataa 660  
 caatttcaca caggaaacag gatctaccat ggccnnbnnb nnnbnnbnnb nnnbnnbnn 720  
 bnnbnnbnnb gggggaggag gatcagcggc cgcaactgat cttcaccaaa cgtattaccg 780  
 ccaggtaaag aaccggaatc cggtgtttac accccgtgaa ggtgcaggaa cgctgaagtt 840  
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 tgtggcgcat gcccgttcgc gtggtctgcg tcgacgcag ccaccagtgc tgcgtcgacg 960  
 ggctattgat gcgctcctgc aggggctgtg tttccactat gacccgctgg ccaaccgcgt 1020  
 ccagtgcctc atcaccacgc tggccattga gtgcggactg gcgacggagt ctgctgccgg 1080  
 aaaactctcc atcaccgcgt ccaccgggc cctgacgttc ctgtcagagc tgggactgat 1140  
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 cagccgtgtg gtatgggaaa acaaacaacg caaaaagcag gggctggata ccctgggcat 1320  
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 gcaagggaact tccccataag gttacaaccg ttcattgtcat aaagcgccat ccgccagcgt 1860  
 tacagggtgc aatgtatctt ttaaacacct gtttatatct cttttaact acttaattac 1920  
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 ccaccgcaag cggcgggccc ctaccggagc cgctttagt tacaactca gacacaacca 2040  
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 ccactccgac cgcgcacaga agctctctca tgggtgaaag cgggtatggt ctggcagggc 2340  
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15

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 26

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26

&lt;210&gt; 27

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 27

ggtagatcct gtttcctgtg tg

22

&lt;210&gt; 28

&lt;211&gt; 110

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

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&lt;222&gt; (37)..(38)

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&lt;221&gt; misc\_feature

&lt;222&gt; (40)..(41)

&lt;223&gt; n = a, g, c or t

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (43)..(44)

&lt;223&gt; n = a, g, c or t

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&lt;222&gt; (46)..(47)

&lt;223&gt; n = a, g, c or t

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nnvnnvnnvn nvnnvnnvnn vnnvnnvnng gccatggtag atcctgtttc 110

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<400> 30  
ggcgctatca tgccataccg 20

18

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accattcggc tagcgatgac

20

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33

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gattggttcg ctgaccattt cc

22

<210> 34  
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<220>  
<223> Primer

<400> 34  
cggcggttacc agaaactcag a

21

<210> 35  
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19

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Primer

&lt;400&gt; 35

aaccgactct gacggcagtt

20

&lt;210&gt; 36

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Peptide

&lt;400&gt; 36

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Gly | Cys | Pro | Thr | Met | Ala | Ala | Arg | Val | Arg | Pro | Val | Leu | Asn | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     | 15  |     |     |

Lys His

&lt;210&gt; 37

&lt;211&gt; 11

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Peptide

&lt;400&gt; 37

|     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Val | Pro | Val | Leu | Met | Ile | Ser | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |

&lt;210&gt; 38

&lt;211&gt; 18

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;220&gt;

&lt;223&gt; Peptide

&lt;400&gt; 38

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Leu | Ser | Thr | Arg | His | His | Asn | Val | Ile | Asp | Arg | Phe | Asn | Leu | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |     |

Asn Phe

20

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<220>  
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1 5 10 15

Ala Asp

<210> 40  
<211> 12  
<212> PRT  
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<220>  
<223> Peptide

<400> 40  
Ala Asn Leu Trp Arg Ile Val Leu His Gly Trp Trp  
1 5 10

<210> 41  
<211> 12  
<212> PRT  
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<220>  
<223> Peptide

<400> 41  
Val Ser Phe Met Leu Leu Gly Pro His Arg His Arg  
1 5 10

<210> 42  
<211> 11  
<212> PRT  
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<220>  
<223> Peptide

21

<400> 42  
Leu Val Leu His Trp Leu Ser Leu Gly Ser Arg  
1 5 10

<210> 43  
<211> 12  
<212> PRT  
<213> Artificial sequence

<220>  
<223> Peptide

<400> 43  
Ser Asn Gln Val Val Leu Ile Leu His Leu Arg Pro  
1 5 10

<210> 44  
<211> 12  
<212> PRT  
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1 5 10

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<400> 45  
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42

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